

Compd #	MOLSTRUCTURE
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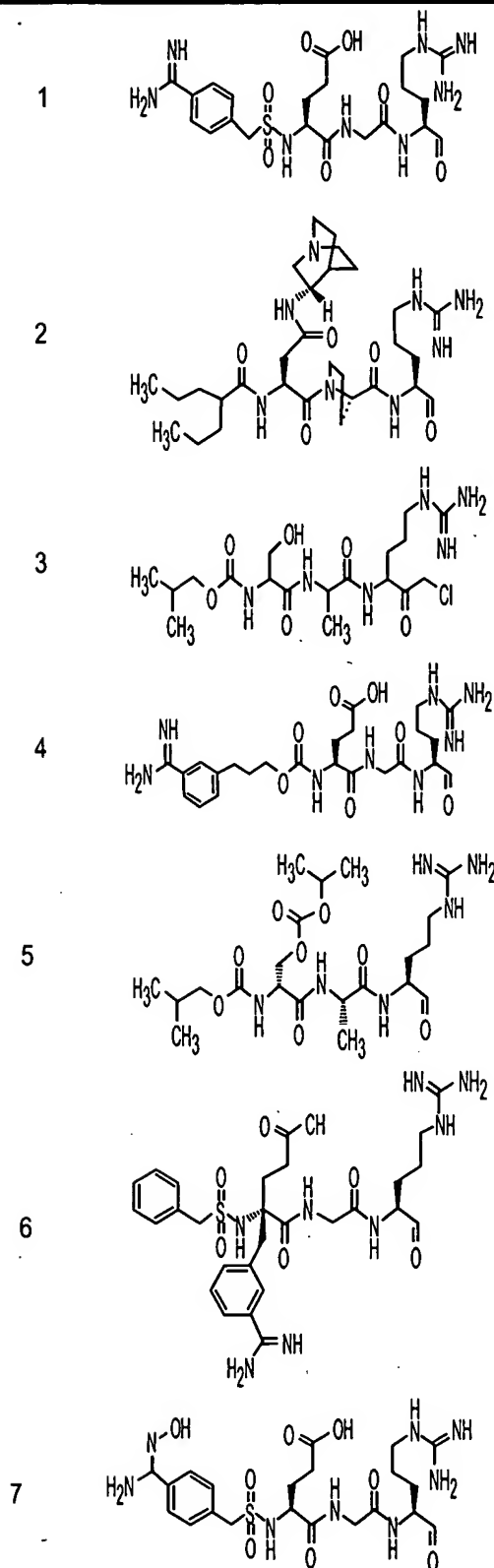


FIG. 1A

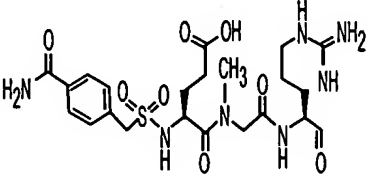
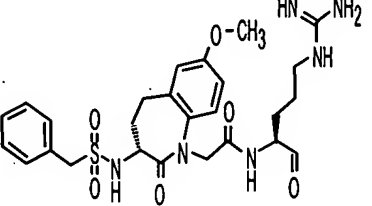
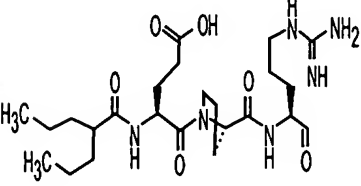
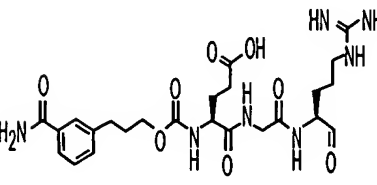
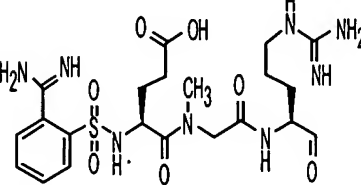
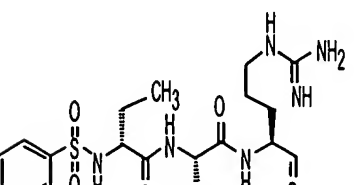
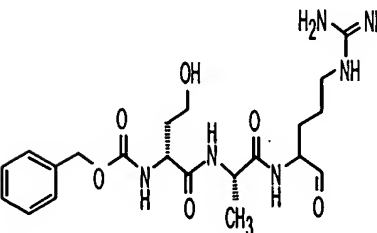
Compd #	MOLSTRUCTURE
8	
9	
10	
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12	
13	
14	

FIG. 1B

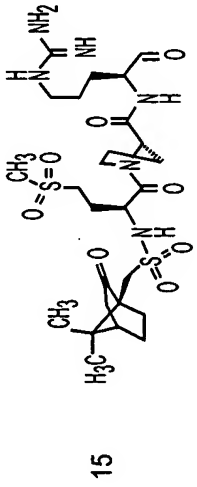
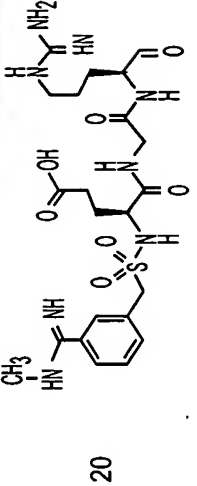
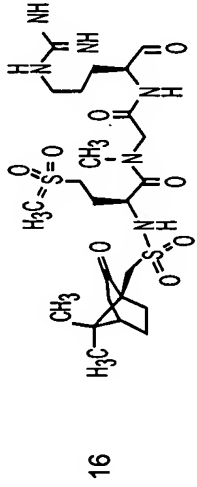
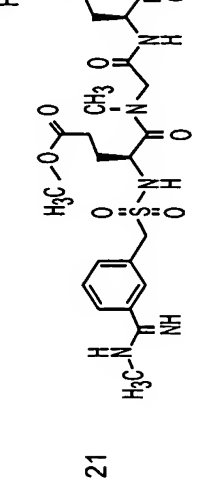
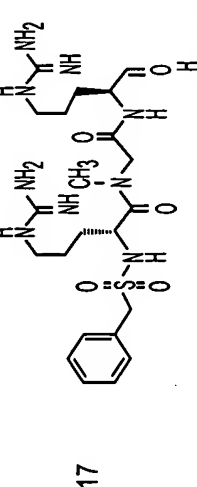
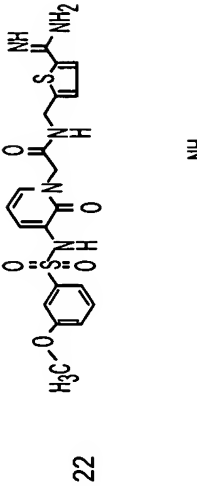
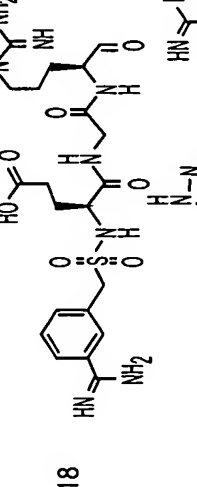
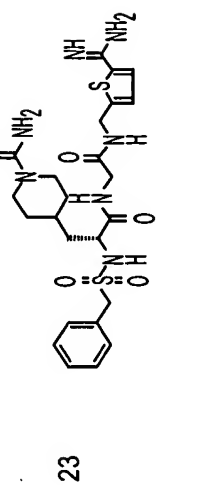
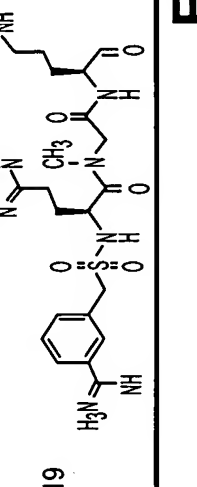
Compd #	MOLSTRUCTURE	Compd #	MOLSTRUCTURE
15		20	
16		21	
17		22	
18		23	
19			

FIG. 1C

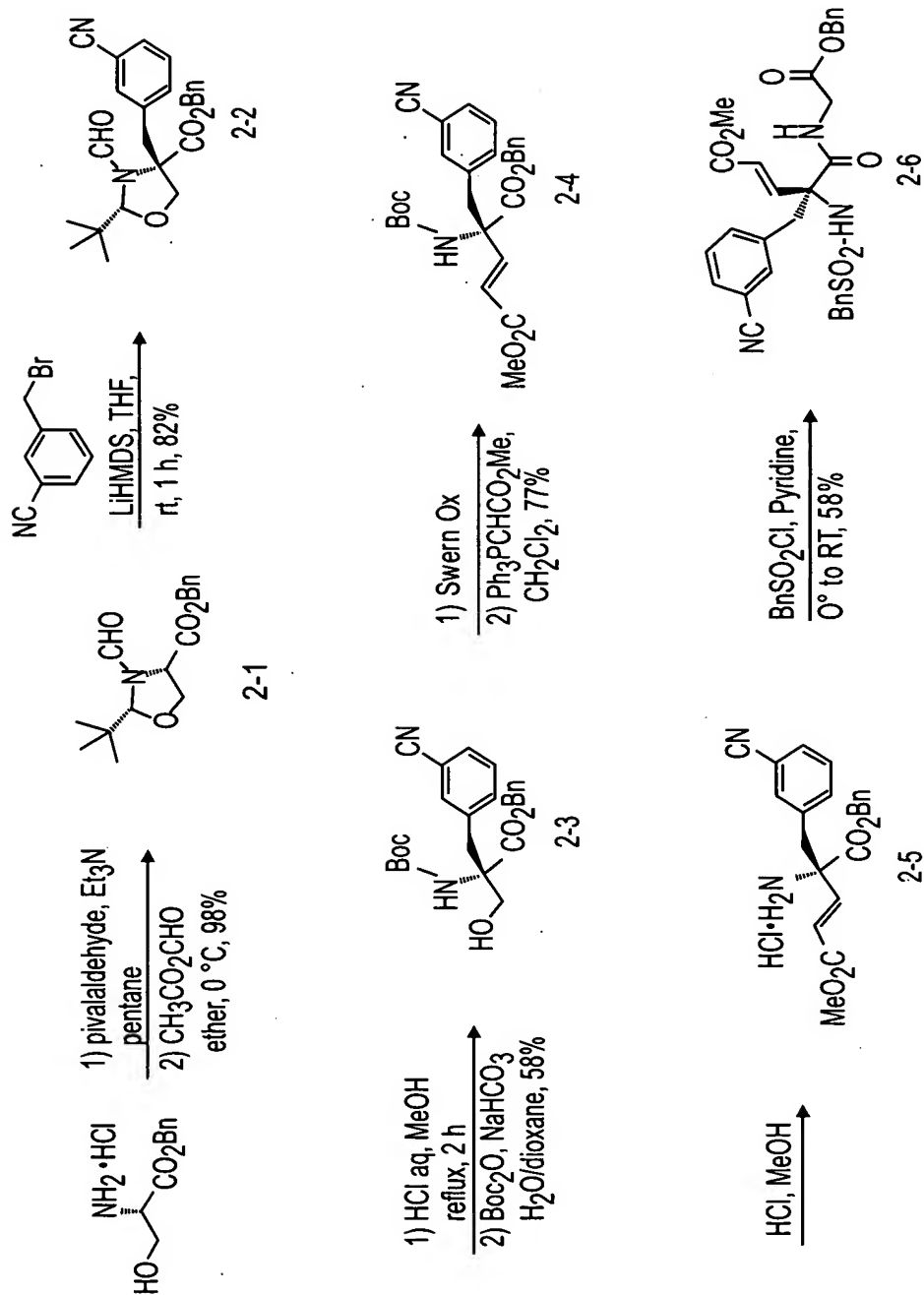


FIG. 2A

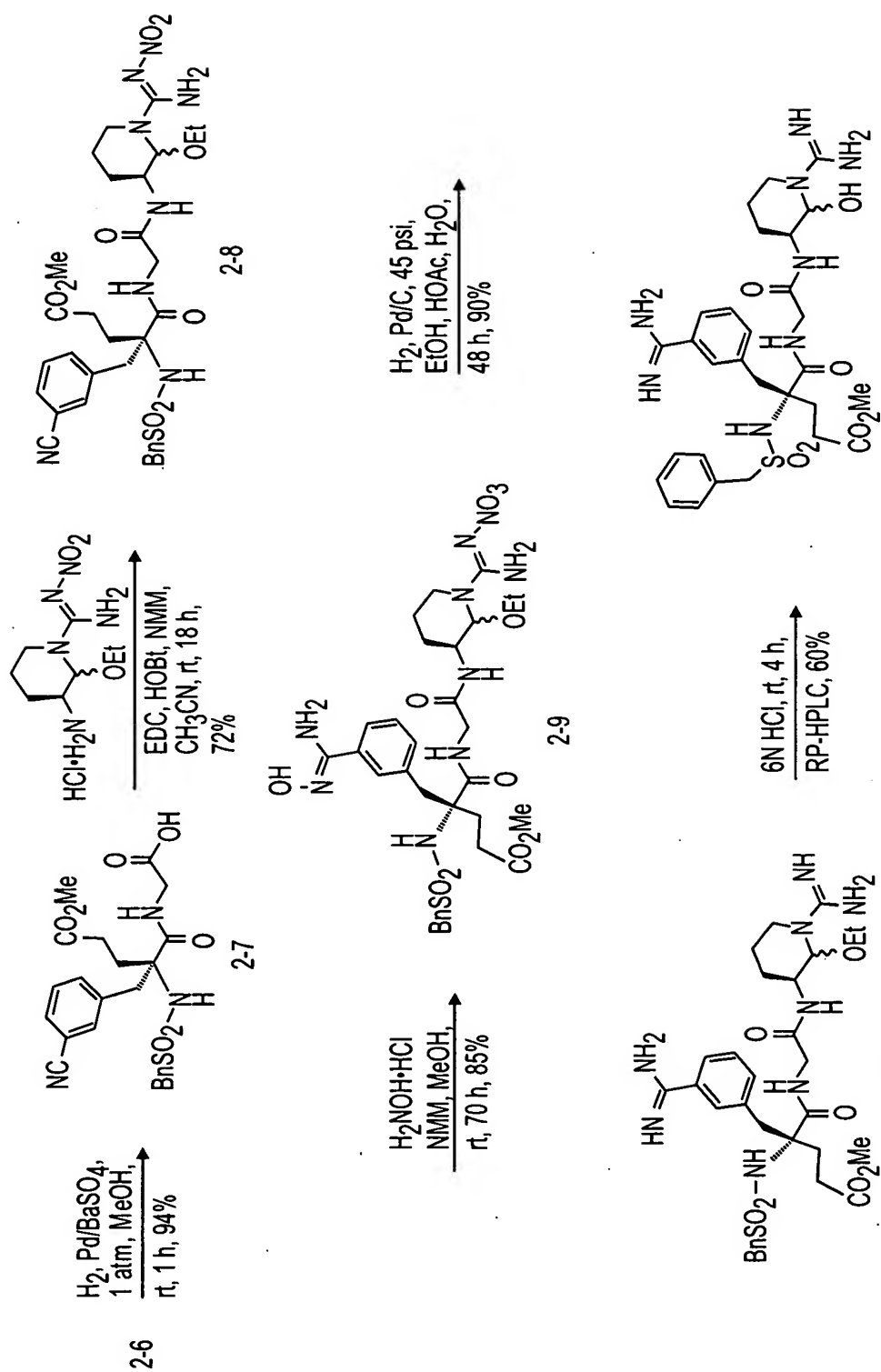


FIG. 2B

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10	20	30	40	50	60
GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT					
CAACAACCCCCGTGCCTACGCCTACTCCCGCTCACCGGGACCGTCCATTTCGGACGTACGA					
V V G G T D A D E G E H P W Q V S L H A>					
70	80	90	100	110	120
CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC					
GACCCGGTCCCGGTGTAGACGCCACGAAGGGAGTAGAGAGGGTTGACCGACCAGAGACGG					
L G Q G H I C G A S L I S P N W L V S A>					
130	140	150	160	170	180
GCACACTGCTACATCGATGACAGAGGATTTCAGGTACTCAGACCCACGCAGTGGACGGCC					
CGTGTGACGATGTAGCTACTGTCTCCTAAGTCCATGAGTCTGGGGTGCGTACCTGCCGG					
A H C Y I D D R G F R Y S D P T Q W T A>					
190	200	210	220	230	240
TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC					
AAGGACCCGAACGTGCTGGTCTCGGTTCGCGTCGCGGGGACCCACGTCCTCGCGTCCGAG					
F L G L H D Q S Q R S A P G V Q E R R L>					
250	260	270	280	290	300
AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG					
TTCGCGTAGTAGAGGGTGGGGAAGAAGTTACTGAAGTGGAAGCTGATACTGTAGCGCGAC					
K R I I S H P F F N D F T F D Y D I A L>					
310	320	330	340	350	360
CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC					
GACCTCGACCTCTTTGGCCGTCTCATGTCGAGGTACCACGCCGGGTAGACGGACGGCCTG					
L E L E K P A E Y S S M V R P I C L P D>					

FIG. 3A

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      370      380      390      400      410      420
GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTACGGGCTGGGGACACACCCAG
CGGAGGGTACAGAAGGGACGGCCGTTCCGGTAGACCCAGTGCCCGACCCCTGTGTGGGTC
  A  S  H  V  F  P  A  G  K  A  I  W  V  T  G  W  G  H  T  Q>

      430      440      450      460      470      480
TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC
ATACCTCCGTGACCGCGCGACTAGGACGTTTTCCCACTCTAGGCGCAGTAGTTGGTCTGG
  Y  G  G  T  G  A  L  I  L  Q  K  G  E  I  R  V  I  N  Q  T>

      490      500      510      520      530      540
ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC
TGGACGCTCTTGGAGGACGGCGTCGTCTAGTGCGGCGCGTACTACACGCACCCGAAGGAG
  T  C  E  N  L  L  P  Q  Q  I  T  P  R  M  M  C  V  G  F  L>

      550      560      570      580      590      600
AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG
TCGCCGCCGCACCTGAGGACGGTCCCACTAAGGCCCCCTGGGGACAGGTGCGACCTCCGC
  S  G  G  V  D  S  C  Q  G  D  S  G  G  P  L  S  S  V  E  A>

      610      620      630      640      650      660
GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC
CTACCCGCCTAGAAGGTCCGGCCACACCACTCGACCCCTCTGCCGACGCGAGTCTCCTTG
  D  G  R  I  F  Q  A  G  V  V  S  W  G  D  G  C  A  Q  R  N>

      670      680      690      700      710      720
AAGCCAGGCGTGACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACTGGG
TTCGGTCCGCACATGTGTTCCGAGGGAGACAAAGCCCTGACCTAGTTTCTCTTGACCC
  K  P  G  V  Y  T  R  L  P  L  F  R  D  W  I  K  E  N  T  G>

```

FIG. 3B

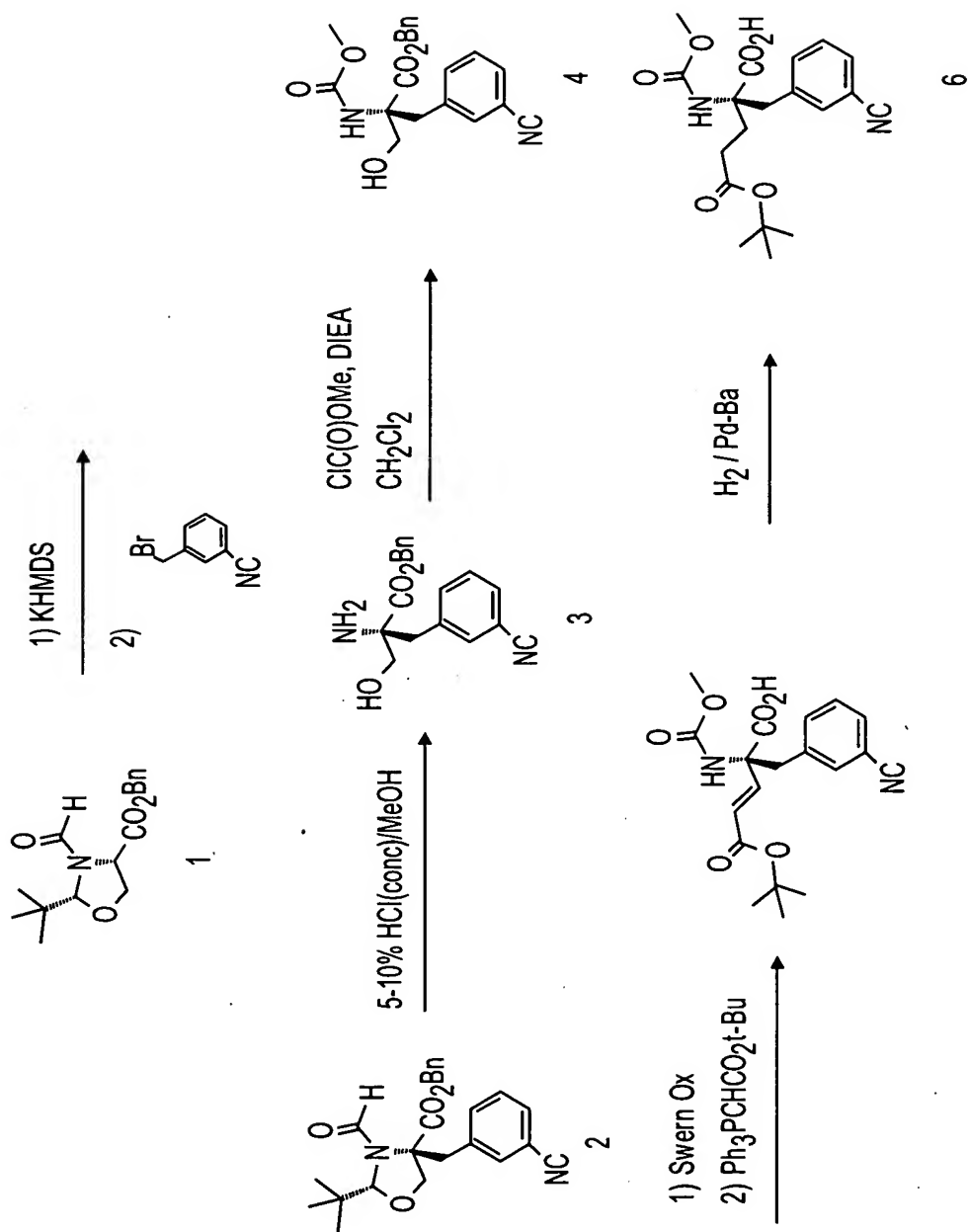
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GTATAG

CATATC

V *>

FIG. 3C



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FIG. 4A

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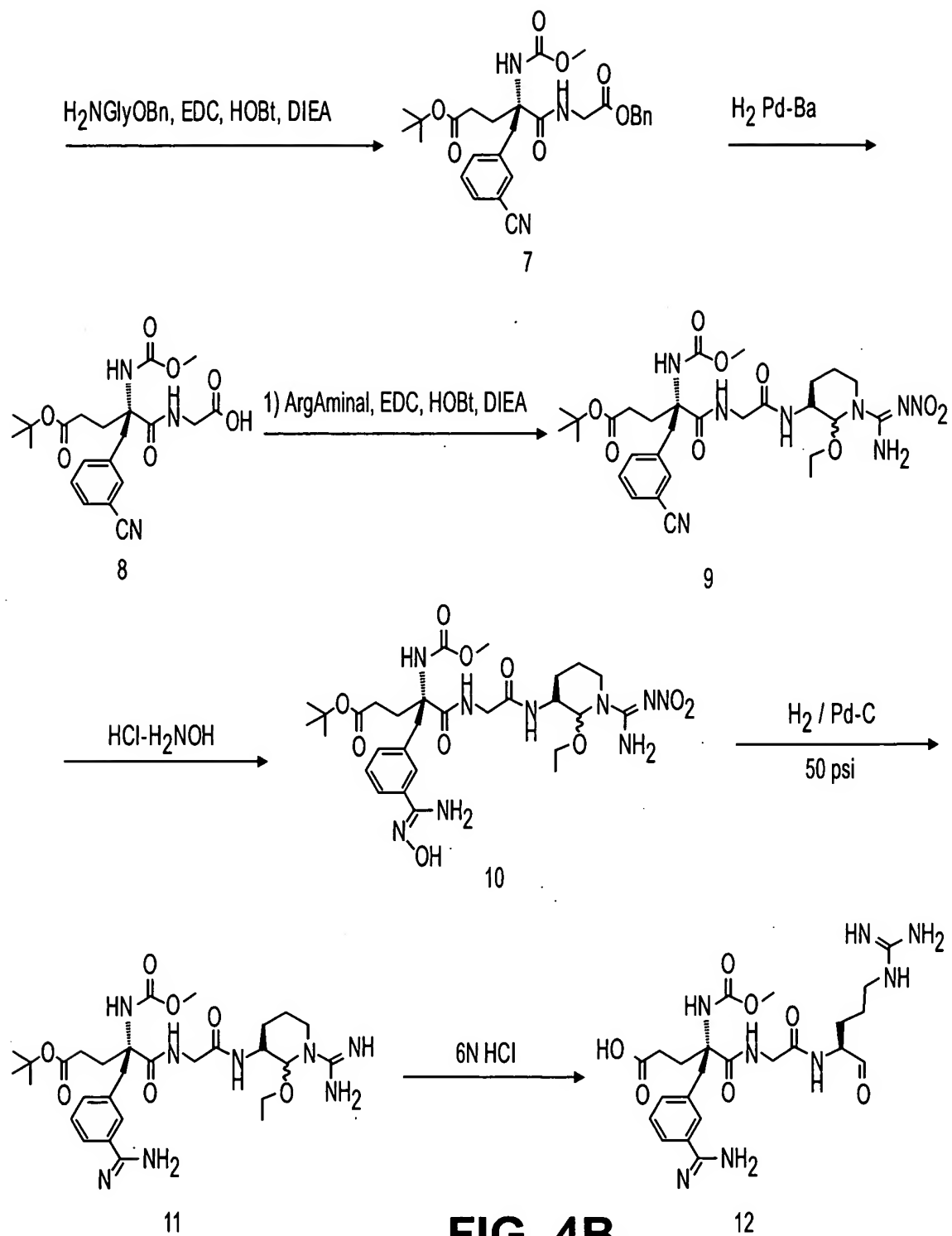


FIG. 4B

REPLACEMENT SHEET

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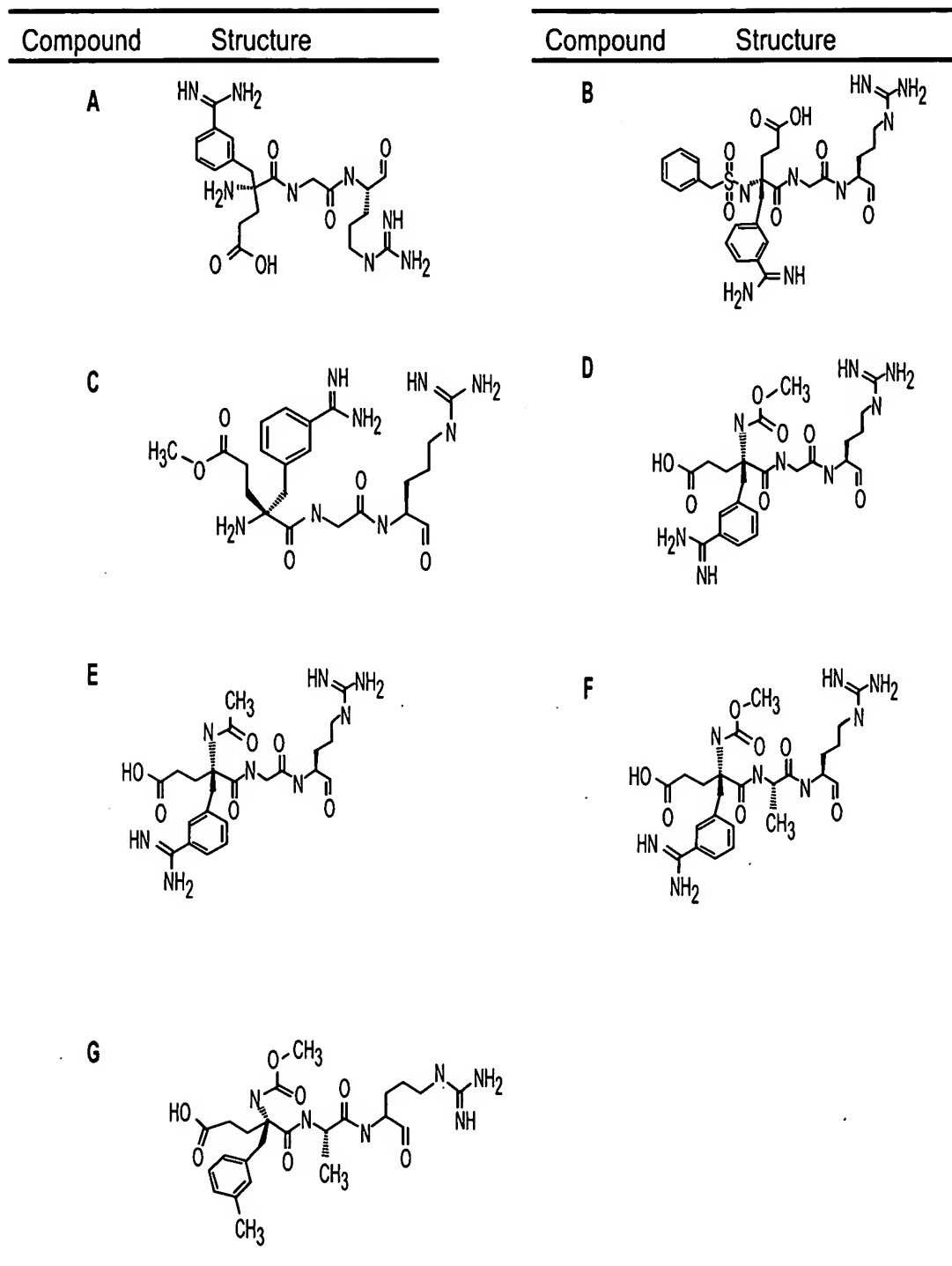


FIG. 5A

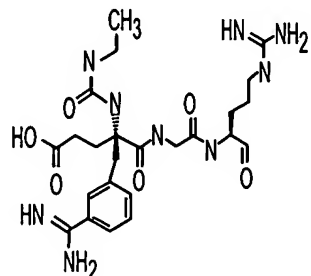
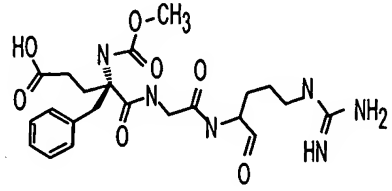
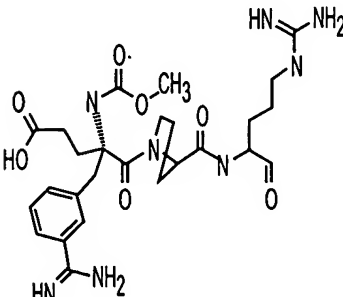
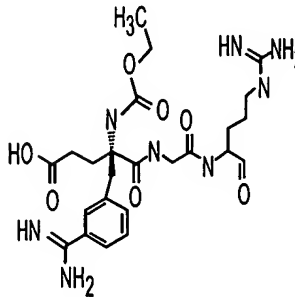
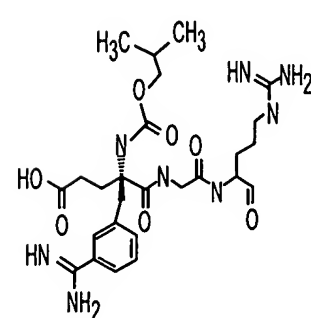
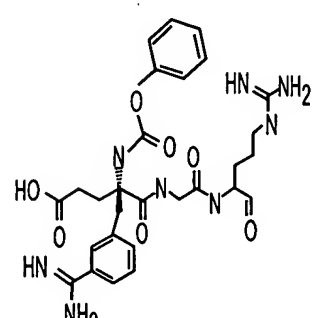
Compound	Structure	Compound	Structure
H		I	
J		K	
L		M	

FIG. 5B